

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2005, 09:11:12 ; Search time 70.6 Seconds  
(without alignments)  
60.260 Million cell updates/sec

Title: US-10-509-620-1  
Perfect score: 57  
Sequence: 1 YGRRARRRRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	57	100.0	11	8	ADG12910	Adg12910 Cytoplasm
2	57	100.0	11	8	ADG12868	Adg12868 Cytoplasm
3	52	91.2	11	8	ADG12912	Adg12912 Cytoplasm
4	52	91.2	11	8	ADG12880	Adg12880 Cytoplasm
5	51	89.5	11	8	ADG12869	Adg12869 Cytoplasm
6	51	89.5	11	8	ADG12908	Adg12908 Cytoplasm
7	50	87.7	21	8	ADG12949	Adg12949 Cytoplasm
8	50	87.7	26	2	AAW76545	Aaw76545 HIV-1 TAT
9	46	80.7	11	2	AAAY25079	Aay25079 Transduct
10	46	80.7	11	3	AAAY93548	Aay93548 Amino aci
11	46	80.7	11	3	AAB29420	Aab29420 Synthetic
12	46	80.7	11	4	AAE05279	Aae05279 Human imm
13	46	80.7	11	5	AAU76086	Aau76086 Peptide t
14	46	80.7	11	6	ABP96986	Abp96986 Anti-infl
15	46	80.7	11	6	ABP56079	Abp56079 Protein t
16	46	80.7	11	6	AAE33885	Aae33885 HIV-Tat s
17	46	80.7	11	7	ADN60174	Adn60174 Novel rec
18	46	80.7	11	8	ADI52956	Adi52956 PTD-7 pep
19	46	80.7	12	2	AAR44186	Aar44186 Anti-herp
20	46	80.7	12	2	AAR44187	Aar44187 Anti-herp
21	45	78.9	10	5	AAU78931	Aau78931 9 Arginin
22	45	78.9	11	2	AAW50263	Aaw50263 HIV-1 tat
23	45	78.9	11	2	AAAY05415	Aay05415 Tat pepti
24	45	78.9	11	2	AAAY25075	Aay25075 TAT trans
25	45	78.9	11	3	AAB27088	Aab27088 Beta-cate
26	45	78.9	11	3	AAB09907	Aab09907 HIV tat p
27	45	78.9	11	3	AAAY93542	Aay93542 Amino aci
28	45	78.9	11	3	AAAY71015	Aay71015 Human imm
29	45	78.9	11	3	AAB35698	Aab35698 Peptide a
30	45	78.9	11	3	AAB03961	Aab03961 Minimal e
31	45	78.9	11	3	AAB29413	Aab29413 HIV TAT t
32	45	78.9	11	3	AAB03932	Aab03932 TAT prote
33	45	78.9	11	4	AAB71757	Aab71757 HIV TAT p
34	45	78.9	11	4	AAB71756	Aab71756 NTR3 deri
35	45	78.9	11	4	AAB60006	Aab60006 Internali
36	45	78.9	11	4	AAE05268	Aae05268 Human imm
37	45	78.9	11	4	AAE02973	Aae02973 Protein t
38	45	78.9	11	4	AAE03418	Aae03418 Human imm
39	45	78.9	11	4	AAE03815	Aae03815 HIV tat p
40	45	78.9	11	4	AAB98683	Aab98683 HIV TAT p
41	45	78.9	11	4	AAB73305	Aab73305 HIV-1 TAT
42	45	78.9	11	4	AAG70458	Aag70458 Human G2
43	45	78.9	11	4	AAG68376	Aag68376 Human Chk
44	45	78.9	11	4	AAG65673	Aag65673 HIV tat p

45	45	78.9	11	4	AAE12605	Aae12605 Human imm
46	45	78.9	11	4	AAB67673	Aab67673 Transduct
47	45	78.9	11	4	AAE03730	Aae03730 Protein t
48	45	78.9	11	4	AAM50221	Aam50221 HIV-1 tat
49	45	78.9	11	4	AAU09932	Aau09932 Human imm
50	45	78.9	11	4	AAE12891	Aae12891 Human imm
51	45	78.9	11	4	AAE13064	Aae13064 Protein t
52	45	78.9	11	4	AAB69170	Aab69170 HIV tat p
53	45	78.9	11	4	AAB70481	Aab70481 HIV TAT p
54	45	78.9	11	4	AAU09812	Aau09812 HIV-1 tat
55	45	78.9	11	4	AAE04300	Aae04300 Human Imm
56	45	78.9	11	4	AAE12204	Aae12204 Membrane
57	45	78.9	11	4	AAB69548	Aab69548 HIV tat p
58	45	78.9	11	4	AAB85847	Aab85847 HIV-1 tat
59	45	78.9	11	4	AAB82757	Aab82757 HIV TAT p
60	45	78.9	11	5	AAU76115	Aau76115 Peptide t
61	45	78.9	11	5	AAU77483	Aau77483 HIV-1 tat
62	45	78.9	11	5	ABG78986	Abg78986 Cell pene
63	45	78.9	11	5	AAE18125	Aae18125 Human imm
64	45	78.9	11	5	ABB74239	Abb74239 HIV TAT f
65	45	78.9	11	5	ABB74244	Abb74244 HIV TAT f
66	45	78.9	11	5	AAE23080	Aae23080 HIV tat p
67	45	78.9	11	5	ABB82413	Abb82413 HIV-1 pep
68	45	78.9	11	5	ABP51634	Abp51634 HIV tat p
69	45	78.9	11	5	AAE20790	Aae20790 Human imm
70	45	78.9	11	5	AAU75548	Aau75548 Human imm
71	45	78.9	11	5	ABB05786	Abb05786 HIV tat r
72	45	78.9	11	5	ABB07211	Abb07211 Amino aci
73	45	78.9	11	5	AAU78967	Aau78967 TAT pepti
74	45	78.9	11	5	AAU77222	Aau77222 HIV tat p
75	45	78.9	11	5	AAM47460	Aam47460 HIV tat p
76	45	78.9	11	5	AAE18343	Aae18343 Human imm
77	45	78.9	11	5	ABB84578	Abb84578 HIV TAT p
78	45	78.9	11	5	ABG95820	Abg95820 Cell pene
79	45	78.9	11	5	AAM48622	Aam48622 Anti-infl
80	45	78.9	11	5	AAM48621	Aam48621 Anti-infl
81	45	78.9	11	5	AAE18833	Aae18833 Protein t
82	45	78.9	11	5	AAU79799	Aau79799 Peptide s
83	45	78.9	11	5	AAU11033	Aau11033 Human imm
84	45	78.9	11	5	AAE21137	Aae21137 HIV Tat p
85	45	78.9	11	5	AAM48194	Aam48194 HIV Tat p
86	45	78.9	11	5	AAE16487	Aae16487 Human imm
87	45	78.9	11	5	ADG27654	Adg27654 Human LGR
88	45	78.9	11	6	AAO16343	Aao16343 Human imm
89	45	78.9	11	6	AAE35420	Aae35420 HIV tat p
90	45	78.9	11	6	ABP57917	Abp57917 Human imm

91	45	78.9	11	6	ABB99504	Abb99504 Amino aci
92	45	78.9	11	6	ABP71286	Abp71286 TAT-deriv
93	45	78.9	11	6	ABG76123	Abg76123 Tat-deriv
94	45	78.9	11	6	ABU09580	Abu09580 Cell perm
95	45	78.9	11	6	ABP96989	Abp96989 Anti-infl
96	45	78.9	11	6	ABP97352	Abp97352 Tat fragm
97	45	78.9	11	6	ABP56074	Abp56074 TAT trans
98	45	78.9	11	6	AAE35355	Aae35355 HIV type
99	45	78.9	11	6	AAE33880	Aae33880 Human imm
100	45	78.9	11	6	ABG74845	Abg74845 HIV TAT p
101	45	78.9	11	6	AAO16688	Aao16688 HIV cell-
102	45	78.9	11	6	ABP70229	Abp70229 Membrane
103	45	78.9	11	6	ABG72698	Abg72698 HIV tat p
104	45	78.9	11	6	AAO26515	Aao26515 FITC-cons
105	45	78.9	11	6	AAE33579	Aae33579 Human imm
106	45	78.9	11	6	AAE36378	Aae36378 Human imm
107	45	78.9	11	6	ABP57670	Abp57670 HIV tat r
108	45	78.9	11	6	ABR61934	Abr61934 Tat pepti
109	45	78.9	11	6	ABR61953	Abr61953 Tat pepti
110	45	78.9	11	6	ADA61897	Ada61897 NFkB esse
111	45	78.9	11	6	ADA61898	Ada61898 NFkB esse
112	45	78.9	11	6	ADA45194	Ada45194 HIV TAT P
113	45	78.9	11	6	ADA50142	Ada50142 HIV-TAT p
114	45	78.9	11	6	ADA61217	Ada61217 HIV tat p
115	45	78.9	11	6	ABR82379	Abr82379 Peptide f
116	45	78.9	11	6	ADA37057	Ada37057 Tat prote
117	45	78.9	11	7	AAO30117	Aao30117 HIV tat p
118	45	78.9	11	7	ADA88841	Ada88841 Antennape
119	45	78.9	11	7	ABR84578	Abr84578 HIV Tat p
120	45	78.9	11	7	AAE38677	Aae38677 HIV Tat d
121	45	78.9	11	7	ADB90670	Adb90670 Internali
122	45	78.9	11	7	ADB99525	Adb99525 TAT pepti
123	45	78.9	11	7	ABR82753	Abr82753 Amino aci
124	45	78.9	11	7	ADC21309	Adc21309 HIV-1 TAT
125	45	78.9	11	7	ADC21301	Adc21301 HIV-1 TAT
126	45	78.9	11	7	ADC35032	Adc35032 HIV Tat-p
127	45	78.9	11	7	ADC42891	Adc42891 HIV tat p
128	45	78.9	11	7	ADD57130	Add57130 HLA bindi
129	45	78.9	11	7	ADD21430	Add21430 HIV-1 TAT
130	45	78.9	11	7	ADD26427	Add26427 transmemb
131	45	78.9	11	7	ADE36734	Ade36734 Internali
132	45	78.9	11	7	ADD90605	Add90605 HIV prote
133	45	78.9	11	7	ADD90779	Add90779 HIV tat p
134	45	78.9	11	7	ADF56534	Adf56534 HIV-1 pro
135	45	78.9	11	7	ADF88578	Adf88578 Protein t
136	45	78.9	11	7	ADG44412	Adg44412 Anti-path

137	45	78.9	11	7	ADG14373	Adg14373 HIV Tat p
138	45	78.9	11	7	ADG17947	Adg17947 FITC cons
139	45	78.9	11	7	ADG28005	Adg28005 HIV TAT p
140	45	78.9	11	7	ADG73133	Adg73133 HIV TAT p
141	45	78.9	11	7	ABW02718	Abw02718 HIV TAT p
142	45	78.9	11	7	ADH78808	Adh78808 Internali
143	45	78.9	11	7	ADL12189	Adl12189 HIV TAT d
144	45	78.9	11	7	ADL88643	Adl88643 HIV TAT p
145	45	78.9	11	7	ADN60167	Adn60167 Novel rec
146	45	78.9	11	8	ADE83322	Ade83322 HIV tat p
147	45	78.9	11	8	ADF12507	Adf12507 HIV TAT p
148	45	78.9	11	8	ADF57558	Adf57558 HIV TAT p
149	45	78.9	11	8	ADG27413	Adg27413 HIV-1 tat
150	45	78.9	11	8	ADF77317	Adf77317 HIV tat p
151	45	78.9	11	8	ADG12882	Adg12882 HIV tat p
152	45	78.9	11	8	ADG12884	Adg12884 Cytoplasm
153	45	78.9	11	8	ADG12870	Adg12870 Cytoplasm
154	45	78.9	11	8	ADG12906	Adg12906 Cytoplasm
155	45	78.9	11	8	ADG74144	Adg74144 HIV TAT p
156	45	78.9	11	8	ADG73688	Adg73688 Protein t
157	45	78.9	11	8	ADJ45759	Adj45759 HIV TAT p
158	45	78.9	11	8	ADJ93635	Adj93635 Tat-deriv
159	45	78.9	11	8	ABU64425	Abu64425 Peptide c
160	45	78.9	11	8	ADJ58092	Adj58092 HIV TAT p
161	45	78.9	11	8	ADI52951	Adi52951 HIV PTD1
162	45	78.9	11	8	ADJ78886	Adj78886 Basic res
163	45	78.9	11	8	ADK15587	Adk15587 Membrane
164	45	78.9	11	8	ADL70729	Adl70729 Fusion po
165	45	78.9	11	8	ADJ95456	Adj95456 HIV TAT p
166	45	78.9	11	8	ADM82987	Adm82987 Transcell
167	45	78.9	11	8	ADJ94771	Adj94771 Internali
168	45	78.9	11	8	ADM68206	Adm68206 Inositol
169	45	78.9	11	8	ADL99095	Adl99095 CFTR inte
170	45	78.9	11	8	ADM94778	Adm94778 HIV tat p
171	45	78.9	11	8	ADN36474	Adn36474 Protein t
172	45	78.9	11	8	ADM57316	Adm57316 Modular a
173	45	78.9	11	8	ADM57317	Adm57317 Modular a
174	45	78.9	11	8	ADO26476	Ado26476 HIV type
175	45	78.9	11	8	ADM96996	Adm96996 HIV TAT p
176	45	78.9	11	8	ADN11632	Adn11632 Calcineur
177	45	78.9	11	8	ADO43337	Ado43337 HIV-1 TAT
178	45	78.9	11	8	ADP49502	Adp49502 Human imm
179	45	78.9	11	8	ADO71466	Ado71466 HIV-1 TAT
180	45	78.9	11	8	ADQ75012	Adq75012 HIV Tat p
181	45	78.9	11	8	ADQ60189	Adq60189 HIV tat p
182	45	78.9	11	8	ADQ88636	Adq88636 TAT prote

183	45	78.9	11	8	ADP95948	Adp95948 HIV-1 TAT
184	45	78.9	11	8	ADQ60107	Adq60107 TAT-deriv
185	45	78.9	11	8	ADQ91934	Adq91934 HIV TAT p
186	45	78.9	11	8	ADS17640	Ads17640 Amino aci
187	45	78.9	11	8	ADR31986	Adr31986 Heat shoc
188	45	78.9	11	8	ADS86878	Ads86878 Protein t
189	45	78.9	11	8	ADT89547	Adt89547 Human imm
190	45	78.9	11	8	ADS17739	Ads17739 HIV-Tat (
191	45	78.9	12	2	AAR44189	Aar44189 Anti-herp
192	45	78.9	12	2	AAR49557	Aar49557 Residues
193	45	78.9	12	2	AAW26450	Aaw26450 Peptide o
194	45	78.9	12	2	AAW31210	Aaw31210 HIV-TAT p
195	45	78.9	12	2	AAW76156	Aaw76156 HIV Type
196	45	78.9	12	2	AAW61334	Aaw61334 Tat pepti
197	45	78.9	12	2	AAW01544	Aay01544 TAT domai
198	45	78.9	12	4	AAB83294	Aab83294 BBB pepti
199	45	78.9	12	4	AAB83295	Aab83295 BBB pepti
200	45	78.9	12	4	AAB70382	Aab70382 HIV Tat p

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OM protein - protein search, using sw model

Run on: June 9, 2005, 09:56:43 ; Search time 18.2 Seconds  
(without alignments)  
45.118 Million cell updates/sec

Title: US-10-509-620-1  
Perfect score: 57  
Sequence: 1 YGRRARRRRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 200 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		%					
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	50	87.7	26	2	US-08-847-176-6	Sequence 6, Appli	
2	48	84.2	12	1	US-08-234-979-1	Sequence 1, Appli	
3	48	84.2	12	2	US-08-473-025-1	Sequence 1, Appli	
4	46	80.7	11	3	US-09-208-966-7	Sequence 7, Appli	
5	46	80.7	11	4	US-09-775-052A-7	Sequence 7, Appli	
6	46	80.7	12	2	US-08-378-709-31	Sequence 31, Appl	
7	45	78.9	11	2	US-08-706-741B-54	Sequence 54, Appl	
8	45	78.9	11	2	US-08-924-695A-54	Sequence 54, Appl	
9	45	78.9	11	3	US-09-208-966-2	Sequence 2, Appli	
10	45	78.9	11	3	US-09-296-089-37	Sequence 37, Appl	
11	45	78.9	11	4	US-09-837-863-2	Sequence 2, Appli	
12	45	78.9	11	4	US-09-660-742-1	Sequence 1, Appli	
13	45	78.9	11	4	US-09-434-345-2	Sequence 2, Appli	
14	45	78.9	11	4	US-09-632-287A-22	Sequence 22, Appl	
15	45	78.9	11	4	US-09-632-277A-4	Sequence 4, Appli	
16	45	78.9	11	4	US-09-612-033B-15	Sequence 15, Appl	
17	45	78.9	11	4	US-09-780-070-37	Sequence 37, Appl	
18	45	78.9	11	4	US-09-775-052A-2	Sequence 2, Appli	
19	45	78.9	11	4	US-09-911-842A-6	Sequence 6, Appli	
20	45	78.9	11	4	US-09-997-465B-2	Sequence 2, Appli	
21	45	78.9	11	4	US-10-083-889-17	Sequence 17, Appl	
22	45	78.9	11	4	US-09-551-976-37	Sequence 37, Appl	
23	45	78.9	11	4	US-09-265-107-75	Sequence 75, Appl	
24	45	78.9	11	4	US-09-724-126A-16	Sequence 16, Appl	
25	45	78.9	11	4	US-09-545-433-14	Sequence 14, Appl	
26	45	78.9	11	4	US-10-031-505-12	Sequence 12, Appl	

27	45	78.9	11	4	US-10-144-549-6	Sequence 6, Appli
28	45	78.9	12	1	US-08-450-257-47	Sequence 47, Appl
29	45	78.9	12	1	US-08-450-246-47	Sequence 47, Appl
30	45	78.9	12	1	US-08-450-098-47	Sequence 47, Appl
31	45	78.9	12	1	US-08-451-233-47	Sequence 47, Appl
32	45	78.9	12	1	US-08-450-236-47	Sequence 47, Appl
33	45	78.9	12	2	US-08-733-505A-50	Sequence 50, Appl
34	45	78.9	12	3	US-08-235-403-47	Sequence 47, Appl
35	45	78.9	12	4	US-09-254-126D-46	Sequence 46, Appl
36	45	78.9	12	4	US-09-656-121-14	Sequence 14, Appl
37	45	78.9	12	4	US-09-656-121-15	Sequence 15, Appl
38	45	78.9	14	5	PCT-US95-06077-4	Sequence 4, Appli
39	45	78.9	14	5	PCT-US95-06077-10	Sequence 10, Appl
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41	45	78.9	14	5	PCT-US95-06077-12	Sequence 12, Appl
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50	45	78.9	15	1	US-08-450-236-5	Sequence 5, Appli
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53	45	78.9	15	3	US-08-235-403-6	Sequence 6, Appli
54	45	78.9	15	4	US-09-911-842A-7	Sequence 7, Appli
55	45	78.9	15	4	US-09-724-126A-17	Sequence 17, Appl
56	45	78.9	16	4	US-09-101-751A-73	Sequence 73, Appl
57	45	78.9	17	2	US-08-902-623-7	Sequence 7, Appli
58	45	78.9	18	4	US-09-720-003C-1	Sequence 1, Appli
59	45	78.9	18	5	PCT-US95-06077-3	Sequence 3, Appli
60	45	78.9	20	4	US-09-720-003C-6	Sequence 6, Appli
61	45	78.9	21	1	US-08-450-257-50	Sequence 50, Appl
62	45	78.9	21	1	US-08-450-246-50	Sequence 50, Appl
63	45	78.9	21	1	US-08-450-098-50	Sequence 50, Appl
64	45	78.9	21	1	US-08-451-233-50	Sequence 50, Appl
65	45	78.9	21	1	US-08-450-236-50	Sequence 50, Appl
66	45	78.9	21	3	US-08-235-403-50	Sequence 50, Appl
67	45	78.9	22	1	US-08-450-257-3	Sequence 3, Appli
68	45	78.9	22	1	US-08-450-246-3	Sequence 3, Appli
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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

### SUMMARIES

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4	46	80.7	11	14	US-10-405-339-17	Sequence 17, Appl
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117	45	78.9	11	17	US-10-758-636A-16	Sequence 16, Appl
118	45	78.9	12	9	US-09-779-791A-4	Sequence 4, Appli
119	45	78.9	12	11	US-09-779-791A-4	Sequence 4, Appli
120	45	78.9	12	13	US-10-024-935-7	Sequence 7, Appli
121	45	78.9	12	14	US-10-229-915-16	Sequence 16, Appl
122	45	78.9	12	14	US-10-405-339-55	Sequence 55, Appl
123	45	78.9	12	14	US-10-405-339-56	Sequence 56, Appl
124	45	78.9	12	15	US-10-353-678-1	Sequence 1, Appli
125	45	78.9	12	15	US-10-603-409-7	Sequence 7, Appli
126	45	78.9	12	16	US-10-341-815-3	Sequence 3, Appli
127	45	78.9	12	16	US-10-756-774-14	Sequence 14, Appl
128	45	78.9	12	16	US-10-756-774-15	Sequence 15, Appl
129	45	78.9	12	16	US-10-722-176A-12	Sequence 12, Appl
130	45	78.9	12	16	US-10-475-024-31	Sequence 31, Appl
131	45	78.9	12	16	US-10-836-804-11	Sequence 11, Appl

132	45	78.9	12	17	US-10-699-562-49	Sequence 49, Appl
133	45	78.9	13	10	US-09-134-793-8	Sequence 8, Appli
134	45	78.9	13	14	US-10-083-815-70	Sequence 70, Appl
135	45	78.9	13	14	US-10-156-570A-30	Sequence 30, Appl
136	45	78.9	13	14	US-10-061-607A-5	Sequence 5, Appli
137	45	78.9	13	16	US-10-165-860A-16	Sequence 16, Appl
138	45	78.9	13	16	US-10-789-102-4	Sequence 4, Appli
139	45	78.9	13	17	US-10-738-632-8	Sequence 8, Appli
140	45	78.9	13	17	US-10-809-144-13	Sequence 13, Appl
141	45	78.9	13	17	US-10-938-249-173	Sequence 173, App
142	45	78.9	14	10	US-09-910-432-3	Sequence 3, Appli
143	45	78.9	14	16	US-10-399-241A-23	Sequence 23, Appl
144	45	78.9	14	16	US-10-281-092-36	Sequence 36, Appl
145	45	78.9	14	16	US-10-790-768A-7	Sequence 7, Appli
146	45	78.9	14	16	US-10-790-768A-8	Sequence 8, Appli
147	45	78.9	15	9	US-09-815-108-10	Sequence 10, Appl
148	45	78.9	15	9	US-09-805-805-9	Sequence 9, Appli
149	45	78.9	15	9	US-09-895-943-14	Sequence 14, Appl
150	45	78.9	15	9	US-09-867-274-24	Sequence 24, Appl
151	45	78.9	15	9	US-09-955-866-25	Sequence 25, Appl
152	45	78.9	15	9	US-09-928-175-26	Sequence 26, Appl
153	45	78.9	15	9	US-09-995-542-14	Sequence 14, Appl
154	45	78.9	15	9	US-09-927-850-19	Sequence 19, Appl
155	45	78.9	15	9	US-09-995-515-15	Sequence 15, Appl
156	45	78.9	15	9	US-09-895-593-14	Sequence 14, Appl
157	45	78.9	15	9	US-09-896-738-21	Sequence 21, Appl
158	45	78.9	15	10	US-09-798-053-11	Sequence 11, Appl
159	45	78.9	15	14	US-10-139-833-19	Sequence 19, Appl
160	45	78.9	15	14	US-10-156-424A-15	Sequence 15, Appl
161	45	78.9	15	14	US-10-146-574-28	Sequence 28, Appl
162	45	78.9	15	14	US-10-229-584-10	Sequence 10, Appl
163	45	78.9	15	14	US-10-156-487A-8	Sequence 8, Appli
164	45	78.9	15	14	US-10-251-947-8	Sequence 8, Appli
165	45	78.9	15	14	US-10-271-697-7	Sequence 7, Appli
166	45	78.9	15	14	US-10-139-947-8	Sequence 8, Appli
167	45	78.9	15	14	US-10-374-207-37	Sequence 37, Appl
168	45	78.9	15	14	US-10-061-607A-48	Sequence 48, Appl
169	45	78.9	15	14	US-10-076-260-7	Sequence 7, Appli
170	45	78.9	15	15	US-10-412-804A-12	Sequence 12, Appl
171	45	78.9	15	15	US-10-373-228-7	Sequence 7, Appli
172	45	78.9	15	16	US-10-758-672A-17	Sequence 17, Appl
173	45	78.9	15	16	US-10-735-354-8	Sequence 8, Appli
174	45	78.9	15	16	US-10-347-145B-110	Sequence 110, App
175	45	78.9	15	17	US-10-485-180-56	Sequence 56, Appl
176	45	78.9	15	17	US-10-745-110-6	Sequence 6, Appli
177	45	78.9	15	17	US-10-758-636A-17	Sequence 17, Appl



178	45	78.9	15	17	US-10-864-774-1	Sequence 1, Appli
179	45	78.9	16	10	US-09-999-724-73	Sequence 73, Appl
180	45	78.9	16	10	US-09-910-432-4	Sequence 4, Appli
181	45	78.9	16	14	US-10-226-956-306	Sequence 306, App
182	45	78.9	16	14	US-10-405-339-38	Sequence 38, Appl
183	45	78.9	16	14	US-10-405-339-51	Sequence 51, Appl
184	45	78.9	16	14	US-10-405-339-59	Sequence 59, Appl
185	45	78.9	16	16	US-10-819-375-120	Sequence 120, App
186	45	78.9	17	10	US-09-847-946A-141	Sequence 141, App
187	45	78.9	17	10	US-09-847-946A-142	Sequence 142, App
188	45	78.9	17	14	US-10-061-607A-43	Sequence 43, Appl
189	45	78.9	18	9	US-09-809-567-17	Sequence 17, Appl
190	45	78.9	18	10	US-09-910-432-5	Sequence 5, Appli
191	45	78.9	18	14	US-10-216-156-17	Sequence 17, Appl
192	45	78.9	18	15	US-10-616-788-17	Sequence 17, Appl
193	45	78.9	18	16	US-10-819-375-117	Sequence 117, App
194	45	78.9	18	16	US-10-347-145B-106	Sequence 106, App
195	45	78.9	19	9	US-09-886-404-14	Sequence 14, Appl
196	45	78.9	19	9	US-09-821-821-25	Sequence 25, Appl
197	45	78.9	19	14	US-10-215-759-5	Sequence 5, Appli
198	45	78.9	19	14	US-10-037-591A-14	Sequence 14, Appl
199	45	78.9	19	14	US-10-264-672-5	Sequence 5, Appli
200	45	78.9	19	15	US-10-383-999-5	Sequence 5, Appli

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OM protein - protein search, using sw model

Run on: June 9, 2005, 09:53:02 ; Search time 12.6 Seconds  
(without alignments)  
83.999 Million cell updates/sec

Title: US-10-509-620-1  
Perfect score: 57  
Sequence: 1 YGRRARRRRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
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1	45	78.9	37 2	S29829		protamine Z3 - sma	
2	45	78.9	47 2	F58208		protamine II-5 - p	
3	45	78.9	47 2	E58208		protamine II-4 - p	
4	41	71.9	45 2	C58208		protamine II-2 - p	
5	41	71.9	45 2	D58208		protamine II-3 - p	
6	41	71.9	45 2	B58208		protamine II-1 - p	
7	40	70.2	49 2	S00228		protamine - horse	
8	40	70.2	49 2	S02007		protamine I - rabb	
9	40	70.2	50 1	HSPG		sperm histone - pi	
10	40	70.2	50 1	HSSH		sperm histone - sh	
11	40	70.2	50 2	S22582		protamine 1 - Sagu	
12	40	70.2	50 2	S21672		protamine 1 - pig	
13	39	68.4	43 2	D58213		protamine III - Am	
14	38	66.7	32 2	B02669		protamine (salmine	
15	37	64.9	41 2	G58208		protamine I - blac	
16	37	64.9	46 2	A18865		protamine Z2 - sma	
17	36	63.2	21 2	PN0082		sperm chromatin pr	
18	35	61.4	30 1	IRTRC2		protamine 1a - rai	
19	35	61.4	31 2	I51349		protamine - rainbo	
20	35	61.4	33 2	D21211		protamine TP17 - r	
21	35	61.4	33 2	C21211		protamine TP16 - r	
22	35	61.4	33 2	T01070		protamine - rainbo	
23	35	61.4	41 2	H58208		protamine II - bla	
24	35	61.4	48 2	S29973		protamine 1 - guin	

25	34	59.6	30	1	CLHR2A	protamine YII - At
26	34	59.6	30	1	CLHRY2	protamine YII - Pa
27	34	59.6	30	1	IRTR4	protamine pTP4 - r
28	34	59.6	30	1	IRTR78	protamine CIII, mi
29	34	59.6	31	1	CLHRZ	protamine Z - Paci
30	34	59.6	31	1	CLHRZA	protamine Z - Atla
31	34	59.6	32	1	IRTR2	protamine II - rai
32	34	59.6	32	1	YZPK1	protamine I - nort
33	34	59.6	33	1	IRTR1A	protamine IA - rai
34	34	59.6	33	1	IRTR1B	protamine IB - rai
35	33	57.9	32	1	SLONA1	protamine AI - chu
36	33	57.9	33	1	IRTR42	protamine 2c - rai
37	33	57.9	33	1	IRTR59	protamine CII - ra
38	33	57.9	33	2	S00710	protamine CII - ch
39	33	57.9	33	2	A21211	protamine TP14 - r
40	33	57.9	33	2	E21211	protamine TP21 - r
41	33	57.9	48	2	A84247	hypothetical prote
42	32.5	57.0	33	2	A26762	protamine (mugilin
43	32.5	57.0	33	2	B26762	protamine (mugilin
44	32	56.1	27	1	SRAPC	protamine B - Russ
45	32	56.1	31	1	CLHR1A	protamine YI - Atl
46	32	56.1	31	1	CLHRY1	protamine YI - Pac
47	32	56.1	34	2	JN0582	protamine (scombri
48	32	56.1	40	2	A40128	probable antigen 1
49	32	56.1	41	2	A58213	protamine - green
50	31	54.4	27	1	SRAPAS	protamine A - stel
51	31	54.4	34	2	S20439	protamine - yellow
52	31	54.4	36	2	JA0173	basic peptide - wi
53	31	54.4	47	2	S22828	protamine - killer
54	30	52.6	25	1	JC4278	ribosomal protein
55	30	52.6	25	1	R6BY4B	ribosomal protein
56	30	52.6	25	2	JQ1617	ribosomal protein
57	30	52.6	25	2	JC4685	ribosomal protein
58	30	52.6	25	2	T38719	ribosomal protein
59	30	52.6	25	2	S38425	ribosomal protein
60	30	52.6	25	2	T49214	ribosomal protein
61	30	52.6	25	2	T06233	ribosomal protein
62	30	52.6	39	1	S28546	protamine 1 - Japa
63	30	52.6	40	1	S14717	protamine 2 - Japa
64	30	52.6	44	2	C48396	ribosomal protein
65	30	52.6	45	2	E86607	L34 ribosomal prot
66	30	52.6	45	2	A72017	ribosomal protein
67	30	52.6	45	2	A90081	50S ribosomal prot
68	29	50.9	30	1	IRTRC3	protamine CIII, ma
69	29	50.9	32	2	F24970	protamine 3a - rai
70	29	50.9	32	2	I51089	protamine - Japane

71	29	50.9	34	1	TYTUZ2	protamine Z2 - blu
72	29	50.9	34	1	TYTUY2	protamine Y2 - blu
73	29	50.9	34	1	TYTUZ1	protamine Z1 - blu
74	29	50.9	34	2	JX0204	protamine Z2 - str
75	29	50.9	34	2	JX0203	protamine Z1 - str
76	29	50.9	44	2	AE2232	50S ribosomal prot
77	29	50.9	50	2	T30417	hypothetical prote
78	28.5	50.0	44	2	E98097	50S ribosomal prot
79	28.5	50.0	44	2	C95233	ribosomal protein
80	28.5	50.0	44	2	C86641	50S ribosomal prot
81	28	49.1	22	2	C64330	ribosomal protein
82	28	49.1	27	2	I44636	homeotic protein H
83	28	49.1	39	2	AE3109	hypothetical prote
84	28	49.1	39	2	I52378	gene HOX B6 protei
85	28	49.1	44	2	H97358	L34 protein [impor
86	28	49.1	45	2	B81733	ribosomal protein
87	28	49.1	45	2	E71470	probable L34 ribos
88	28	49.1	47	2	G70316	ribosomal protein
89	27	47.4	32	2	D87579	hypothetical prote
90	27	47.4	36	1	JU0352	4.6K protein - Chl
91	27	47.4	37	1	R5LV36	ribosomal protein
92	27	47.4	37	2	E97596	hypothetical prote
93	27	47.4	43	2	B97505	hypothetical prote
94	27	47.4	44	2	AG1431	ribosomal protein
95	27	47.4	44	2	AE1805	ribosomal protein
96	27	47.4	45	2	JQ0738	ribosomal protein
97	27	47.4	45	2	B84158	ribosomal protein
98	27	47.4	48	2	E64251	ribosomal protein
99	26.5	46.5	50	2	AH2496	transposase asr715
100	26	45.6	18	2	PS0387	platelet-derived g
101	26	45.6	39	2	T28154	histone H3 homolog
102	26	45.6	44	1	R6BS34	ribosomal protein
103	26	45.6	44	1	R6PS34	ribosomal protein
104	26	45.6	44	2	H81370	50S ribosomal prot
105	26	45.6	44	2	A82951	50S ribosomal prot
106	26	45.6	44	2	G81027	50S ribosomal prot
107	26	45.6	44	2	I40651	ribosomal protein
108	26	45.6	44	2	F87344	ribosomal protein
109	26	45.6	45	2	H82375	ribosomal protein
110	26	45.6	46	2	B82517	50S ribosomal prot
111	26	45.6	46	2	T06965	ribosomal protein
112	26	45.6	46	2	A72805	gp43.1 protein - M
113	25	43.9	16	2	A35552	caldesmon - turkey
114	25	43.9	21	2	PS0146	histone H1 - sea u
115	25	43.9	23	2	S60566	homeodomain protei
116	25	43.9	31	2	S00685	hypothetical prote

117	25	43.9	31	2	E70202	hypothetical prote
118	25	43.9	33	2	A87213	hypothetical prote
119	25	43.9	33	2	A41822	antimicrobial pept
120	25	43.9	41	2	S52323	major core protein
121	25	43.9	42	2	D95059	hypothetical prote
122	25	43.9	43	2	PS0359	hypothetical prote
123	25	43.9	44	2	AC3544	LSU ribosomal prot
124	25	43.9	46	2	E85743	hypothetical prote
125	25	43.9	47	2	C87299	hypothetical prote
126	25	43.9	48	2	AH3067	hypothetical prote
127	25	43.9	49	2	D65197	hypothetical 5.2 k
128	25	43.9	50	2	E82529	hypothetical prote
129	24	42.1	14	2	PC1215	homeotic protein E
130	24	42.1	17	2	A34835	ribosomal protein
131	24	42.1	27	2	I44629	homeotic protein H
132	24	42.1	27	2	A44616	homeotic protein H
133	24	42.1	27	2	H48200	homeotic protein H
134	24	42.1	27	2	G48200	homeotic protein H
135	24	42.1	27	2	F48200	homeotic protein H
136	24	42.1	27	2	B44616	homeotic protein H
137	24	42.1	27	2	F44616	homeotic protein H
138	24	42.1	27	2	G44616	homeotic protein H
139	24	42.1	27	2	I48200	homeotic protein H
140	24	42.1	27	2	G44636	homeotic protein H
141	24	42.1	27	2	F44636	homeotic protein H
142	24	42.1	28	2	S51593	myrB protein - Mic
143	24	42.1	29	2	T34643	hypothetical prote
144	24	42.1	30	2	S48114	cystic fibrosis tr
145	24	42.1	31	2	H72808	gp82.2 protein - M
146	24	42.1	34	2	I65264	homeotic protein H
147	24	42.1	37	2	T07519	ribosomal protein
148	24	42.1	37	2	F45186	homeotic protein G
149	24	42.1	38	2	C83729	hypothetical prote
150	24	42.1	42	2	S49217	ribosomal protein
151	24	42.1	42	2	I65241	homeotic protein H
152	24	42.1	43	2	E82271	hypothetical prote
153	24	42.1	44	2	E64107	ribosomal protein
154	24	42.1	46	1	R5EC34	ribosomal protein
155	24	42.1	46	2	A48542	CRF-related diuret
156	24	42.1	46	2	AH0957	50s ribosomal prot
157	24	42.1	46	2	H86054	50S ribosomal subu
158	24	42.1	46	2	F91208	50S ribosomal subu
159	24	42.1	46	2	B30474	homeotic protein H
160	24	42.1	47	1	JQ0732	ribosomal protein
161	24	42.1	48	2	S78287	ribosomal protein
162	24	42.1	48	2	C25979	nodulation protein

163	24	42.1	50	2	T11759	hypothetical prote
164	24	42.1	50	2	S48115	cystic fibrosis tr
165	24	42.1	50	2	S10907	homeotic protein (
166	23	40.4	23	2	S43765	ribosomal protein
167	23	40.4	26	2	S33869	ribosomal protein
168	23	40.4	28	1	G9BPSV	gene 9 protein - s
169	23	40.4	29	2	S32734	homeotic protein -
170	23	40.4	30	2	B82290	hypothetical prote
171	23	40.4	32	2	A41270	protamine S4 - sma
172	23	40.4	34	2	I65263	homeobox protein H
173	23	40.4	36	2	A60146	65K heat shock pro
174	23	40.4	39	2	A61127	adrenocorticotropi
175	23	40.4	39	2	A01459	corticotropin - os
176	23	40.4	41	2	F84007	hypothetical prote
177	23	40.4	42	2	S05710	homeotic protein c
178	23	40.4	42	2	T36238	hypothetical prote
179	23	40.4	44	2	G64700	ribosomal protein
180	23	40.4	44	2	AD0992	hypothetical prote
181	23	40.4	44	2	H90641	hypothetical prote
182	23	40.4	44	2	H85492	hypothetical prote
183	23	40.4	44	2	D64732	hypothetical prote
184	23	40.4	45	2	A83765	hypothetical prote
185	23	40.4	47	1	JC1154	ribosomal protein
186	23	40.4	47	2	E84931	50S ribosomal prot
187	23	40.4	47	2	T29970	hypothetical prote
188	23	40.4	48	2	H82871	ribosomal protein
189	23	40.4	48	2	S73486	ribosomal protein
190	23	40.4	48	2	A57125	polyphenolic adhes
191	23	40.4	49	2	A37334	L-lactate dehydrog
192	23	40.4	49	2	T12228	ABA-stress ripenin
193	23	40.4	50	2	C69094	ribosomal protein
194	22	38.6	20	2	PC4387	GroEL protein homo
195	22	38.6	20	2	I65242	homeotic protein H
196	22	38.6	21	2	B35417	30K serine protein
197	22	38.6	21	2	I58423	arylhydrocarbon re
198	22	38.6	23	2	S45031	homeotic protein S
199	22	38.6	24	2	S16111	cathepsin G (EC 3.
200	22	38.6	27	2	JT0517	Ig heavy chain V-I

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OM protein - protein search, using sw model

Run on: June 9, 2005, 09:14:02 ; Search time 57.8 Seconds  
(without alignments)  
97.455 Million cell updates/sec

Title: US-10-509-620-1  
Perfect score: 57  
Sequence: 1 YGRRARRRRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	% Query			DB	ID	Description
	No.	Score	Match Length			
1	45	78.9	37 1	PRT3	SCYCA	P30258 scyliorhinu
2	45	78.9	47 2	Q7LZA7		Q7lza7 chrysemys p
3	45	78.9	47 2	Q7LZA9		Q7lza9 chrysemys p
4	43	75.4	50 1	HSP1	HYLLA	P35306 hylobates l
5	41	71.9	45 2	Q7LZB0		Q7lzb0 chrysemys p
6	41	71.9	45 2	Q7LZB1		Q7lzb1 chrysemys p
7	41	71.9	45 2	Q7LZB5		Q7lzb5 chrysemys p
8	41	71.9	48 1	HSP1	HIPCO	Q8wnz8 hipposidero
9	40	70.2	28 1	HSP4	OCTVU	P83216 octopus vul
10	40	70.2	39 2	Q9PRX5		Q9prx5 xenopus lae
11	40	70.2	47 1	HSP1	DESRO	Q8wme4 desmodus ro

12	40	70.2	47	1	HSP1_MONRE	Q7jh06 monophyllus
13	40	70.2	47	1	HSP1_MORME	Q8wnz5 mormoops me
14	40	70.2	47	1	HSP1_PTEPA	Q7jh07 pteronotus
15	40	70.2	48	1	HSP1_PTEHP	Q8wnz9 pteropus hy
16	40	70.2	48	1	HSP1_RHIHA	Q8wnz6 rhinopoma h
17	40	70.2	49	1	HSP1_HORSE	P15341 equus cabal
18	40	70.2	49	1	HSP1_PIG	P04101 sus scrofa
19	40	70.2	49	1	HSP1_RABIT	P10119 oryctolagus
20	40	70.2	49	1	HSP1_SAGIM	P24714 saguinus im
21	40	70.2	49	1	HSP1_TRAPH	Q8mhz2 trachypithe
22	40	70.2	50	1	HSP1_BOVIN	P02318 bos taurus
23	40	70.2	50	1	HSP1_CAPHI	P67833 capra hircu
24	40	70.2	50	1	HSP1_MACMU	Q9gu4 macaca mula
25	40	70.2	50	1	HSP1_MOUSE	P02319 mus musculu
26	40	70.2	50	1	HSP1_PAPCY	Q7jix8 papio cynoc
27	40	70.2	50	1	HSP1_RAT	P10118 rattus norv
28	40	70.2	50	1	HSP1_SHEEP	P68038 ovis aries
29	40	70.2	50	1	HSP1_TRACR	Q9gkq2 trachypithe
30	40	70.2	50	1	HSP1_TRAFR	Q9gkq4 trachypithe
31	40	70.2	50	1	HSP1_TRAGE	Q7jhm8 trachypithe
32	40	70.2	50	1	HSP1_TRAOB	Q7jix9 trachypithe
33	40	70.2	50	1	HSP1_TRAPL	Q7jhm9 trachypithe
34	40	70.2	50	2	Q66QC7	Q66qc7 equus asinu
35	40	70.2	50	2	Q8CEM2	Q8cem2 mus musculu
36	39	68.4	30	1	HSP5_OCTVU	P83217 octopus vul
37	39	68.4	43	2	Q7LZB7	Q7lzb7 alligator m
38	37	64.9	37	2	Q9IM08	Q9im08 bovine herp
39	37	64.9	41	2	Q7LZA8	Q7lza8 elaphe obso
40	37	64.9	45	1	PRT2_SCYCA	P06841 scyliorhinu
41	37	64.9	47	2	Q8V7B9	Q8v7b9 tt virus. o
42	37	64.9	50	1	HSP1_HUMAN	P04553 homo sapien
43	36	63.2	21	2	Q7M3Z3	Q7m3z3 illex argen
44	36	63.2	50	1	HSP1_COLBA	Q8mjt0 colobus bad
45	36	63.2	50	1	HSP1_COLGU	Q9gkq5 colobus gue
46	36	63.2	50	1	HSP1_NASLA	Q9gkq3 nasalis lar
47	36	63.2	50	1	HSP1_TRAJO	Q8mjs8 trachypithe
48	35	61.4	30	1	PRTB_ONCMY	P12819 oncorhynchu
49	35	61.4	32	1	PRT7_ONCMY	P08146 oncorhynchu
50	35	61.4	32	1	PRT9_ONCMY	P08147 oncorhynchu
51	35	61.4	41	2	Q7LZA6	Q7lza6 elaphe obso
52	35	61.4	41	2	Q8AEX0	Q8aex0 human immun
53	35	61.4	44	2	O13030	O13030 cynops pyrr
54	35	61.4	45	1	HSP1_CHABE	Q8wny9 chalinolobu
55	35	61.4	45	1	HSP1_EPTBN	Q8wmd3 eptesicus b
56	35	61.4	45	1	HSP1_PIPSA	Q7jh04 pipistrellu
57	35	61.4	46	1	HSP1_MYODA	Q8wny8 myotis daub



58	35	61.4	46	2	Q64412	Q64412 cavia porce
59	35	61.4	47	1	HSP1_CAVPO	P35304 cavia porce
60	35	61.4	47	1	HSP1_EPTBR	Q8wmc7 eptesicus b
61	35	61.4	47	1	HSP1_EPTFU	Q7jh05 eptesicus f
62	35	61.4	47	1	HSP1_MURCY	Q8wny7 murina cycl
63	35	61.4	47	1	HSP1_PLETO	Q8wnz0 plecotus to
64	35	61.4	49	1	HSP1_NATMI	Q8wnz4 natalus mic
65	35	61.4	49	1	HSP1_PLEAU	Q8wnz1 plecotus au
66	35	61.4	49	1	HSP1_SEMEN	Q9gjr3 semnopithec
67	35	61.4	49	1	HSP1_TRAVT	Q7jiy0 trachypithe
68	35	61.4	49	2	Q8V7C1	Q8v7c1 tt virus. o
69	35	61.4	49	2	Q8V7C2	Q8v7c2 tt virus. o
70	35	61.4	49	2	Q8V7C3	Q8v7c3 tt virus. o
71	35	61.4	50	1	HSP1_PANTR	P35309 pan troglod
72	35	61.4	50	2	Q9GKQ0	Q9gkq0 ateles sp.
73	34	59.6	24	1	HSP3_OCTVU	P83215 octopus vul
74	34	59.6	30	1	PRT1_CLUPA	P02335 clupea pall
75	34	59.6	30	1	PRT3_ONCMY	P02332 oncorhynchu
76	34	59.6	30	1	PRT4_ONCMY	P02333 oncorhynchu
77	34	59.6	31	1	PRT2_CLUPA	P02336 clupea pall
78	34	59.6	32	1	PRI3_ONCMY	P02330 oncorhynchu
79	34	59.6	32	1	PRT1_ESOLU	P02325 esox lucius
80	34	59.6	33	1	PRI1_ONCMY	P02326 oncorhynchu
81	34	59.6	33	1	PRI2_ONCMY	P02328 oncorhynchu
82	34	59.6	46	1	HSP1_CYNVA	Q8wp00 cynocephalu
83	34	59.6	48	2	Q64841	Q64841 human adeno
84	34	59.6	48	2	Q6VGU8	Q6vgu8 human adeno
85	34	59.6	48	2	Q71BX0	Q71bx0 human adeno
86	34	59.6	49	1	HSP1_NATST	Q8wnz3 natalus str
87	34	59.6	49	1	HSP1_PANPA	P35308 pan paniscu
88	34	59.6	49	1	HSP1_SAI SC	Q9gkq1 saimiri sci
89	33	57.9	25	1	RL41_AGABI	P78569 agaricus bi
90	33	57.9	27	2	Q867D2	Q867d2 bos taurus
91	33	57.9	32	1	PRT1_ONCKE	P02327 oncorhynchu
92	33	57.9	32	1	PRT5_ONCMY	P02334 oncorhynchu
93	33	57.9	32	1	PRT6_ONCMY	P08145 oncorhynchu
94	33	57.9	32	1	PRT8_ONCMY	P12817 oncorhynchu
95	33	57.9	45	2	P72155	P72155 pseudomonas
96	33	57.9	48	2	Q9HR17	Q9hr17 halobacteri
97	33	57.9	49	2	Q6TMA9	Q6tma9 coprinus ci
98	33	57.9	50	2	Q7TLQ5	Q7tlq5 choristoneu
99	32.5	57.0	33	1	PRTB_MUGCE	P08130 mugil cepha
100	32	56.1	27	1	PRTB_ACIGU	P02323 acipenser g
101	32	56.1	31	1	PRT3_CLUPA	P02337 clupea pall
102	32	56.1	34	1	PRT1_SCOSC	P83264 scomber sco
103	32	56.1	34	1	PRT2_SCOSC	P83265 scomber sco

104	32	56.1	35	2	Q7S181	Q7s181 neurospora
105	32	56.1	41	2	Q8VLI4	Q8vli4 streptococc
106	32	56.1	41	2	Q8VLI5	Q8vli5 streptococc
107	32	56.1	41	2	Q7LZB3	Q7lzb3 anolis caro
108	32	56.1	44	2	Q8VL77	Q8vl77 streptococc
109	32	56.1	44	2	Q8VLL4	Q8vll4 streptococc
110	32	56.1	44	2	Q8VT74	Q8vt74 streptococc
111	32	56.1	46	2	Q62IU0	Q62iu0 burkholderi
112	32	56.1	47	2	Q7ZSZ6	Q7zsz6 rhea americ
113	32	56.1	47	2	Q802S4	Q802s4 rhea americ
114	32	56.1	47	2	Q802S5	Q802s5 pterocnemias
115	32	56.1	48	2	Q9DF91	Q9df91 apteryx aus
116	32	56.1	49	1	HSP1_OTOHE	Q8wnz2 otonycteris
117	32	56.1	49	2	Q9DF86	Q9df86 crypturellu
118	31.5	55.3	44	2	Q7NKK3	Q7nkk3 gloeobacter
119	31	54.4	21	2	Q9JG23	Q9jg23 tt virus. o
120	31	54.4	21	2	Q9JG30	Q9jg30 tt virus. o
121	31	54.4	27	1	PRTA_ACIST	P02324 acipenser s
122	31	54.4	34	1	PRT_PERFV	P29629 perca flave
123	31	54.4	35	2	Q9ANP3	Q9anp3 bradyrhizob
124	31	54.4	36	2	Q7M1X1	Q7m1x1 cucurbita m
125	31	54.4	37	1	REV_SIVM2	P08809 simian immu
126	31	54.4	37	2	Q6TK89	Q6tk89 acanthosicy
127	31	54.4	37	2	Q90W10	Q90w10 primolius m
128	31	54.4	37	2	Q90W11	Q90w11 cyanopsitta
129	31	54.4	37	2	Q90Y48	Q90y48 cyanopsitta
130	31	54.4	39	2	Q9BPP8	Q9bpp8 bombyx mori
131	31	54.4	39	2	Q9PXW1	Q9pxw1 simian immu
132	31	54.4	41	2	Q6TK75	Q6tk75 praecitrull
133	31	54.4	41	2	Q6TK76	Q6tk76 sechium edu
134	31	54.4	41	2	Q6TK77	Q6tk77 sicyos angu
135	31	54.4	41	2	Q6TK78	Q6tk78 trichosanth
136	31	54.4	41	2	Q6TK79	Q6tk79 luffa grave
137	31	54.4	41	2	Q6TK80	Q6tk80 luffa echin
138	31	54.4	41	2	Q6TK81	Q6tk81 cucurbita p
139	31	54.4	41	2	Q6TK82	Q6tk82 benincasa h
140	31	54.4	41	2	Q6TK83	Q6tk83 luffa quinq
141	31	54.4	41	2	Q6TK84	Q6tk84 marah orega
142	31	54.4	41	2	Q6TK85	Q6tk85 echinocysti
143	31	54.4	41	2	Q6TK86	Q6tk86 lagenaria l
144	31	54.4	41	2	Q6TK87	Q6tk87 citrullus l
145	31	54.4	41	2	Q6TK88	Q6tk88 citrullus c
146	31	54.4	41	2	Q6TK90	Q6tk90 bryonia dio
147	31	54.4	41	2	Q6TK91	Q6tk91 coccinia pa
148	31	54.4	41	2	Q6TK92	Q6tk92 diplocyclos
149	31	54.4	41	2	Q6TK93	Q6tk93 ecballium e

150	31	54.4	41	2	Q90ZS1	Q90zs1 phylloscopu
151	31	54.4	41	2	Q90ZS2	Q90zs2 phylloscopu
152	31	54.4	41	2	Q8AWG3	Q8awg3 lanius excu
153	31	54.4	43	2	Q9DFA5	Q9dfa5 buteo buteo
154	31	54.4	44	1	RL34_THEMA	P58288 thermotoga
155	31	54.4	45	2	Q66PH8	Q66ph8 streptomyce
156	31	54.4	45	2	Q9DF92	Q9df92 anas platyr
157	31	54.4	46	1	HSP1_ORCOR	P24713 orcinus orc
158	31	54.4	46	2	Q65X76	Q65x76 oryza sativ
159	31	54.4	46	2	Q9DF94	Q9df94 acryllium v
160	31	54.4	48	1	RL34_THEAQ	Q7x515 thermus aqu
161	31	54.4	48	2	Q856G4	Q856g4 mycobacteri
162	31	54.4	48	2	Q804F5	Q804f5 lanius meri
163	31	54.4	48	2	Q804F6	Q804f6 lanius sphe
164	31	54.4	48	2	Q804F7	Q804f7 lanius coll
165	31	54.4	48	2	Q804F8	Q804f8 lanius meri
166	31	54.4	48	2	Q804F9	Q804f9 lanius meri
167	31	54.4	49	2	Q9DFA6	Q9dfa6 buteo jamai
168	31	54.4	50	1	HSP1_GORGO	P35303 gorilla gor
169	31	54.4	50	1	HSP1_PONPY	P35310 pongo pygma
170	31	54.4	50	2	Q86690	Q86690 abutilon mo
171	30	52.6	23	2	Q7PF75	Q7pf75 anopheles g
172	30	52.6	25	1	RL41_ARATH	P62120 arabidopsis
173	30	52.6	25	1	RL41_ASHGO	Q75ah3 ashbya goss
174	30	52.6	25	1	RL41_CYPCA	Q6ylx4 cyprinus ca
175	30	52.6	25	1	RL41_EPICO	Q71h53 epinephelus
176	30	52.6	25	1	RL41_FELCA	P62946 felis silve
177	30	52.6	25	1	RL41_FUGRU	P62949 fugu rubrip
178	30	52.6	25	1	RL41_GOSHI	P62122 gossypium h
179	30	52.6	25	1	RL41_HORVU	P62124 hordeum vul
180	30	52.6	25	1	RL41_HUMAN	P62945 homo sapien
181	30	52.6	25	1	RL41_MOUSE	P62947 mus musculu
182	30	52.6	25	1	RL41_ORYSA	P62125 oryza sativ
183	30	52.6	25	1	RL41_PEA	P62123 pisum sativ
184	30	52.6	25	1	RL41_QUESU	O82713 quercus sub
185	30	52.6	25	1	RL41_RAT	P62948 rattus norv
186	30	52.6	25	1	RL41_SCHPO	Q9y710 schizosacch
187	30	52.6	25	1	RL41_SOYBN	O49224 glycine max
188	30	52.6	25	1	RL41_SPOFR	Q7kf89 spodoptera
189	30	52.6	25	1	RL41_TOBAC	P62121 nicotiana t
190	30	52.6	25	1	RL41_YEAST	P05746 saccharomyc
191	30	52.6	25	2	Q962S2	Q962s2 drosophila
192	30	52.6	25	2	Q6B8B3	Q6b8b3 ixodes paci
193	30	52.6	25	2	Q6SZL7	Q6szl7 rhodococcus
194	30	52.6	27	2	Q38560	Q38560 bacterioph
195	30	52.6	35	2	Q62A44	Q62a44 burkholderi

196	30	52.6	39	1	PRT1_BUFJA	P24641 bufo japoni
197	30	52.6	39	1	PRT2_BUFJA	P24642 bufo japoni
198	30	52.6	44	1	RL34_BACST	P23376 bacillus st
199	30	52.6	45	1	RL34_CHLPN	Q9z6x1 chlamydia p
200	30	52.6	45	1	RL34_STAAM	P66252 staphylococ

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OM protein - protein search, using sw model

Run on: June 9, 2005, 14:18:51 ; Search time 82.8 Seconds  
(without alignments)  
51.381 Million cell updates/sec

Title: US-10-509-620-14  
Perfect score: 57  
Sequence: 1 YRRRRRRRRRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score						
1	57	100.0	11	8	ADG	12881	Adg12881 Cytoplasm
2	57	100.0	11	8	ADG	12914	Adg12914 Cytoplasm
3	52	91.2	28	4	AAM	19464	Aam19464 Peptide #
4	52	91.2	28	4	ABB	38931	Abb38931 Peptide #
5	52	91.2	28	4	AAM	32414	Aam32414 Peptide #
6	52	91.2	28	4	ABB	23919	Abb23919 Protein #
7	52	91.2	28	4	AAM	72152	Aam72152 Human bon
8	52	91.2	28	4	AAM	59582	Aam59582 Human bra
9	52	91.2	28	4	ABG	53838	Abg53838 Human liv
10	52	91.2	28	5	ABG	41966	Abg41966 Human pep
11	51	89.5	11	2	AAY	25079	Aay25079 Transduct
12	51	89.5	11	3	AAY	93548	Aay93548 Amino aci
13	51	89.5	11	3	AAB	29420	Aab29420 Synthetic
14	51	89.5	11	4	AAE	05279	Aae05279 Human imm
15	51	89.5	11	5	AAU	76086	Aau76086 Peptide t
16	51	89.5	11	6	ABP	96986	Abp96986 Anti-infl
17	51	89.5	11	6	ABP	56079	Abp56079 Protein t
18	51	89.5	11	6	AAE	33885	Aae33885 HIV-Tat s
19	51	89.5	11	7	ADN	60174	Adn60174 Novel rec
20	51	89.5	11	8	ADI	52956	Adi52956 PTD-7 pep
21	50	87.7	10	2	AAR	44182	Aar44182 Anti-herp
22	50	87.7	10	2	AAR	70516	Aar70516 Anti-cyto
23	50	87.7	10	2	AAW	24824	Aaw24824 Anti-cyto
24	50	87.7	10	2	AAW	25628	Aaw25628 Peptide #
25	50	87.7	10	5	AAM	48650	Aam48650 Anti-infl
26	50	87.7	10	6	ABP	96998	Abp96998 Anti-infl
27	50	87.7	10	6	ADA	61948	Ada61948 NFkB esse
28	50	87.7	10	7	ADA	88910	Ada88910 Internali
29	50	87.7	10	7	ADE	11604	Adel1604 Trojan pr
30	50	87.7	10	8	ADL	99100	Adl99100 CFTR inte
31	50	87.7	11	2	AAW	24825	Aaw24825 Anti-cyto
32	50	87.7	11	2	AAW	25629	Aaw25629 Peptide #
33	50	87.7	11	5	ABP	54078	Abp54078 Transport
34	50	87.7	11	5	AAE	22208	Aae22208 Cationic
35	50	87.7	11	5	AAM	48651	Aam48651 Anti-infl
36	50	87.7	11	6	ABP	96999	Abp96999 Anti-infl
37	50	87.7	11	6	ADA	61949	Ada61949 NFkB esse
38	50	87.7	11	6	ADA	61944	Ada61944 NFkB esse

39	50	87.7	11	6	ADA45193	Ada45193 Protein t
40	50	87.7	11	7	ADC19822	Adc19822 Fluoresce
41	50	87.7	11	7	ADD21429	Add21429 Protein t
42	50	87.7	11	8	ADG12912	Adg12912 Cytoplasm
43	50	87.7	11	8	ADG12880	Adg12880 Cytoplasm
44	50	87.7	11	8	ADR21206	Adr21206 Novel cel
45	50	87.7	12	2	AAR27776	Aar27776 Transacti
46	50	87.7	12	2	AAW24826	Aaw24826 Anti-cyto
47	50	87.7	12	2	AAW25630	Aaw25630 Peptide #
48	50	87.7	12	2	AAW57994	Aaw57994 TAR bindi
49	50	87.7	12	4	AAG79077	Aag79077 Peptide w
50	50	87.7	12	6	ABP97000	Abp97000 Anti-infl
51	50	87.7	12	6	AAE33909	Aae33909 Secretion
52	50	87.7	12	7	ADA88911	Ada88911 Internali
53	50	87.7	12	7	ADE11605	Adel1605 Trojan pr
54	50	87.7	12	8	ADL99101	Adl99101 CFTR inte
55	50	87.7	13	4	AAB70242	Aab70242 Positivel
56	50	87.7	13	5	ABP54102	Abp54102 Transport
57	50	87.7	13	6	AAE33910	Aae33910 Secretion
58	50	87.7	13	7	ADC19907	Adc19907 Homo-D ar
59	50	87.7	14	6	AAE33911	Aae33911 Secretion
60	50	87.7	15	4	AAG79076	Aag79076 Peptide w
61	50	87.7	15	5	AAO20442	Aao20442 N-termina
62	50	87.7	15	6	AAE33912	Aae33912 Secretion
63	50	87.7	16	6	AAE33913	Aae33913 Secretion
64	50	87.7	16	7	ADE11606	Adel1606 Trojan pr
65	50	87.7	17	6	AAE33914	Aae33914 Secretion
66	50	87.7	17	8	ADH76874	Adh76874 Peptide w
67	50	87.7	18	6	AAE33915	Aae33915 Secretion
68	50	87.7	19	5	ABP54103	Abp54103 Transport
69	50	87.7	19	6	AAE33916	Aae33916 Secretion
70	50	87.7	19	7	ADC19908	Adc19908 Homo-D ar
71	50	87.7	19	8	ADH76872	Adh76872 Peptide w
72	50	87.7	20	5	AAE28375	Aae28375 Peptide #
73	50	87.7	20	6	ABP59411	Abp59411 Self-asse
74	50	87.7	20	6	ABP59410	Abp59410 Self-asse
75	50	87.7	20	6	AAE33917	Aae33917 Secretion
76	50	87.7	20	7	ADH44249	Adh44249 Cationic
77	50	87.7	20	8	ADF12139	Adf12139 Transfect
78	50	87.7	20	8	ADF54690	Adf54690 PNA compo
79	50	87.7	21	6	AAE33918	Aae33918 Secretion
80	50	87.7	22	6	AAE33919	Aae33919 Secretion
81	50	87.7	23	2	AAW76542	Aaw76542 HIV-1 TAT
82	50	87.7	23	2	AAW76559	Aaw76559 HIV-1 TAT
83	50	87.7	24	4	ABB43181	Abb43181 Peptide #
84	50	87.7	24	4	AAM37018	Aam37018 Peptide #

85	50	87.7	24	4	AAM76911	Aam76911 Human bon
86	50	87.7	24	4	AAM64090	Aam64090 Human bra
87	50	87.7	24	4	ABG58577	Abg58577 Human liv
88	50	87.7	26	8	ADN11633	Adn11633 Calcineur
89	50	87.7	27	8	ADN11634	Adn11634 Calcineur
90	50	87.7	30	6	ABP59424	Abp59424 Self-asse
91	50	87.7	30	6	ABP59428	Abp59428 Self-asse
92	50	87.7	30	6	ABP59425	Abp59425 Self-asse
93	50	87.7	30	6	ADA49673	Ada49673 Fusion pe
94	50	87.7	30	6	ADA49675	Ada49675 Fusion pe
95	50	87.7	32	5	AAU99806	Aau99806 Biomembra
96	50	87.7	39	4	AAM16480	Aam16480 Peptide #
97	50	87.7	39	4	ABB35465	Abb35465 Peptide #
98	50	87.7	39	4	AAM28970	Aam28970 Peptide #
99	50	87.7	39	4	ABB30298	Abb30298 Peptide #
100	50	87.7	39	4	ABB20902	Abb20902 Protein #
101	50	87.7	39	4	AAM68663	Aam68663 Human bon
102	50	87.7	39	4	AAM56286	Aam56286 Human bra
103	50	87.7	39	4	ABG50324	Abg50324 Human liv
104	50	87.7	39	4	AAM04207	Aam04207 Peptide #
105	50	87.7	39	5	ABG38243	Abg38243 Human pep
106	50	87.7	41	6	ABR61912	Abr61912 Amino aci
107	50	87.7	41	6	ABR61914	Abr61914 Amino aci
108	50	87.7	41	8	ABO54033	Abo54033 Human gen
109	50	87.7	49	8	ABO57271	Abo57271 Human gen
110	50	87.7	50	8	ABO53775	Abo53775 Human gen
111	48	84.2	13	2	AAW24442	Aaw24442 Nucleic a
112	48	84.2	13	5	AAU98549	Aau98549 Peptide l
113	48	84.2	13	6	ABU63057	Abu63057 Peptide l
114	48	84.2	14	2	AAW07678	Aaw07678 BIV TAR a
115	48	84.2	14	2	AAW07673	Aaw07673 HIV RRE I
116	48	84.2	23	2	AAW76543	Aaw76543 HIV-1 TAT
117	47	82.5	14	2	AAW07672	Aaw07672 RRE IIB a
118	47	82.5	14	2	AAW07677	Aaw07677 BIV TAR a
119	47	82.5	26	8	ABO59420	Abo59420 Human gen
120	47	82.5	29	8	ABO56454	Abo56454 Human gen
121	47	82.5	41	4	AAM16780	Aam16780 Peptide #
122	47	82.5	41	4	ABB35764	Abb35764 Peptide #
123	47	82.5	41	4	AAM29265	Aam29265 Peptide #
124	47	82.5	41	4	ABB30600	Abb30600 Peptide #
125	47	82.5	41	4	ABB21188	Abb21188 Protein #
126	47	82.5	41	4	AAM68954	Aam68954 Human bon
127	47	82.5	41	4	AAM56574	Aam56574 Human bra
128	47	82.5	41	4	ABG50617	Abg50617 Human liv
129	47	82.5	41	4	AAM04497	Aam04497 Peptide #
130	47	82.5	41	5	ABG38540	Abg38540 Human pep

131	46	80.7	11	8	ADM57316	Adm57316 Modular a
132	46	80.7	14	2	AAW07676	Aaw07676 BIV TAR a
133	46	80.7	14	2	AAW07675	Aaw07675 BIV TAR a
134	46	80.7	15	2	AAR27777	Aar27777 Transacti
135	46	80.7	23	2	AAW76557	Aaw76557 HIV-1 TAT
136	46	80.7	23	2	AAW76560	Aaw76560 HIV-1 TAT
137	46	80.7	23	2	AAW76544	Aaw76544 HIV-1 TAT
138	46	80.7	23	2	AAW76553	Aaw76553 HIV-1 TAT
139	46	80.7	23	2	AAW76550	Aaw76550 HIV-1 TAT
140	46	80.7	23	2	AAW76549	Aaw76549 HIV-1 TAT
141	46	80.7	23	2	AAW76554	Aaw76554 HIV-1 TAT
142	46	80.7	23	2	AAW76558	Aaw76558 HIV-1 TAT
143	46	80.7	23	2	AAW76551	Aaw76551 HIV-1 TAT
144	46	80.7	37	2	AAW76548	Aaw76548 HIV-1 TAT
145	45	78.9	9	2	AAR24012	Aar24012 Transacti
146	45	78.9	9	2	AAR44181	Aar44181 Anti-herp
147	45	78.9	9	2	AAR57118	Aar57118 Compositi
148	45	78.9	9	2	AAR70518	Aar70518 Anti-cyto
149	45	78.9	9	2	AAR70515	Aar70515 Anti-cyto
150	45	78.9	9	2	AAW24823	Aaw24823 Anti-cyto
151	45	78.9	9	2	AAW25606	Aaw25606 Peptide #
152	45	78.9	9	2	AAW25632	Aaw25632 Peptide #
153	45	78.9	9	2	AAW25627	Aaw25627 Peptide #
154	45	78.9	9	2	AAW67311	Aaw67311 Peptide w
155	45	78.9	9	4	AAU00807	Aau00807 Arginine
156	45	78.9	9	5	ABP54748	Abp54748 Arginine
157	45	78.9	9	5	ABP54753	Abp54753 Arginine
158	45	78.9	9	5	AAM48649	Aam48649 Anti-infl
159	45	78.9	9	5	AAE16152	Aae16152 Arginine
160	45	78.9	9	6	ABP96997	Abp96997 Anti-infl
161	45	78.9	9	6	AAO16669	Aao16669 Cell-perm
162	45	78.9	9	6	ABR44173	Abr44173 Self cell
163	45	78.9	9	6	ABR61935	Abr61935 Amino aci
164	45	78.9	9	6	ABR61954	Abr61954 Amino aci
165	45	78.9	9	7	AAE38688	Aae38688 R9 peptid
166	45	78.9	9	7	ADC42899	Adc42899 Cellular
167	45	78.9	9	7	ADC38642	Adc38642 L-arginin
168	45	78.9	9	7	ADE01160	Ade01160 Human typ
169	45	78.9	9	7	ADF50717	Adf50717 Nona-L-ar
170	45	78.9	9	8	ADH31291	Adh31291 Silicon-b
171	45	78.9	9	8	ADH89694	Adh89694 Cell pene
172	45	78.9	9	8	ADM68208	Adm68208 Inositol
173	45	78.9	9	8	ADM06873	Adm06873 Polyargin
174	45	78.9	9	8	ADQ26227	Adq26227 Transport
175	45	78.9	9	8	ADR21205	Adr21205 Novel cel
176	45	78.9	9	8	ADR50666	Adr50666 Membrane



177	45	78.9	9 8	ADR31966	Adr31966 Heat shoc
178	45	78.9	9 8	ADR82243	Adr82243 Cell perm
179	45	78.9	10 4	AAG87715	Aag87715 Saccharom
180	45	78.9	10 5	AAU78931	Aau78931 9 Arginin
181	45	78.9	10 7	ADC22449	Adc22449 Protein-d
182	45	78.9	10 7	ADC22450	Adc22450 Protein-d
183	45	78.9	10 8	ADG27418	Adg27418 HIV-1 tat
184	45	78.9	10 8	ADK39819	Adk39819 PNA molec
185	45	78.9	10 8	ADK39875	Adk39875 PNA molec
186	45	78.9	10 8	ABU64430	Abu64430 Peptide c
187	45	78.9	10 8	ADK51185	Adk51185 Polynucle
188	45	78.9	11 2	ADE25449	Ade25449 GPIIb/III
189	45	78.9	11 2	ADH59034	Adh59034 GPIIb/IIa
190	45	78.9	11 3	AAY54939	Aay54939 Peptide l
191	45	78.9	11 6	AAE33908	Aae33908 Secretion
192	45	78.9	12 2	AAR26396	Aar26396 Sequence
193	45	78.9	12 2	AAW11093	Aaw11093 Platelet-
194	45	78.9	12 2	AAW31141	Aaw31141 Platelet-
195	45	78.9	13 2	AAR28139	Aar28139 Cell-to-c
196	45	78.9	13 2	AAW52104	Aaw52104 Targettin
197	45	78.9	13 5	ABG95804	Abg95804 Cell pene
198	45	78.9	13 6	AAO16672	Aao16672 Cell-perm
199	45	78.9	13 6	ABB82927	Abb82927 R9-tat pr
200	45	78.9	13 7	ADE11621	Ade11621 HIV-1R-TA

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OM protein - protein search, using sw model

Run on: June 9, 2005, 14:56:46 ; Search time 22 Seconds  
(without alignments)  
37.325 Million cell updates/sec

Title: US-10-509-620-14  
Perfect score: 57  
Sequence: 1 YRRRRRRRRRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result		Query					
No.	Score	Match	Length	DB	ID	Description	
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1	51	89.5	11 3	US-09-208-966-7	Sequence 7, Appli		
2	51	89.5	11 4	US-09-775-052A-7	Sequence 7, Appli		
3	50	87.7	10 1	US-08-332-518-24	Sequence 24, Appl		
4	50	87.7	10 2	US-08-378-709-24	Sequence 24, Appl		
5	50	87.7	11 1	US-08-332-518-25	Sequence 25, Appl		
6	50	87.7	11 2	US-08-378-709-25	Sequence 25, Appl		
7	50	87.7	12 1	US-08-332-518-26	Sequence 26, Appl		
8	50	87.7	12 1	US-08-357-056-12	Sequence 12, Appl		
9	50	87.7	12 1	US-08-475-583-12	Sequence 12, Appl		
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11	50	87.7	13 4	US-09-625-570-5	Sequence 5, Appli		
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13	50	87.7	15 4	US-09-396-195-9	Sequence 9, Appli		
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15	50	87.7	20 3	US-09-083-259-10	Sequence 10, Appl		
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Run on: June 9, 2005, 15:10:02 ; Search time 71.6 Seconds  
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58.892 Million cell updates/sec

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Perfect score: 57  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 483280

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	51	89.5	11	16	US-10-688-299-6	Sequence 6, Appli	
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OM protein - protein search, using sw model

Run on: June 9, 2005, 14:50:15 ; Search time 15 Seconds  
(without alignments)  
70.559 Million cell updates/sec

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	50	87.7	43	2	D58213	protamine III - Am
3	50	87.7	45	2	B58208	protamine II-1 - p
4	46	80.7	48	2	S29973	protamine 1 - guin
5	46	80.7	50	2	S22582	protamine 1 - Sagu
6	45	78.9	45	2	C58208	protamine II-2 - p
7	45	78.9	45	2	D58208	protamine II-3 - p
8	45	78.9	47	2	F58208	protamine II-5 - p
9	45	78.9	47	2	E58208	protamine II-4 - p
10	44	77.2	21	2	PN0082	sperm chromatin pr
11	43	75.4	33	2	D21211	protamine TP17 - r
12	43	75.4	33	2	C21211	protamine TP16 - r
13	43	75.4	33	2	T01070	protamine - rainbo
14	42	73.7	49	2	S00228	protamine - horse
15	42	73.7	49	2	S02007	protamine I - rabb
16	42	73.7	50	1	HSPG	sperm histone - pi
17	42	73.7	50	1	HSSH	sperm histone - sh
18	42	73.7	50	2	S21672	protamine 1 - pig
19	40	70.2	41	2	G58208	protamine I - blac

20	39	68.4	27	1	SRAPC	protamine B - Russ
21	39	68.4	30	1	CLHR2A	protamine YII - At
22	39	68.4	30	1	CLHRY2	protamine YII - Pa
23	39	68.4	31	1	CLHRZ	protamine Z - Paci
24	39	68.4	31	1	CLHRZA	protamine Z - Atla
25	39	68.4	32	1	IRTR2	protamine II - rai
26	39	68.4	32	1	SLONA1	protamine AI - chu
27	39	68.4	32	2	B02669	protamine (salmine
28	39	68.4	33	1	IRTR1A	protamine IA - rai
29	39	68.4	33	1	IRTR42	protamine 2c - rai
30	39	68.4	33	1	IRTR59	protamine CII - ra
31	39	68.4	33	2	S00710	protamine CII - ch
32	39	68.4	33	2	A21211	protamine TP14 - r
33	39	68.4	33	2	E21211	protamine TP21 - r
34	38	66.7	30	1	IRTR78	protamine CIII, mi
35	38	66.7	30	1	IRTRC2	protamine Ia - rai
36	38	66.7	30	1	IRTRC3	protamine CIII, ma
37	38	66.7	31	2	I51349	protamine - rainbo
38	38	66.7	32	1	YZPK1	protamine I - nort
39	38	66.7	32	2	F24970	protamine 3a - rai
40	38	66.7	34	2	S20439	protamine - yellow
41	38	66.7	41	2	A58213	protamine - green
42	37.5	65.8	34	1	TYTUZ2	protamine Z2 - blu
43	37.5	65.8	34	1	TYTUZ1	protamine Z1 - blu
44	37.5	65.8	34	2	JN0582	protamine (scombri
45	37.5	65.8	34	2	JX0204	protamine Z2 - str
46	37.5	65.8	34	2	JX0203	protamine Z1 - str
47	37	64.9	27	1	SRAPAS	protamine A - stel
48	37	64.9	31	1	CLHR1A	protamine YI - Atl
49	37	64.9	31	1	CLHRY1	protamine YI - Pac
50	37	64.9	33	1	IRTR1B	protamine IB - rai
51	37	64.9	33	2	A26762	protamine (mugilin
52	37	64.9	33	2	B26762	protamine (mugilin
53	37	64.9	46	2	A18865	protamine Z2 - sma
54	36.5	64.0	32	2	I51089	protamine - Japane
55	36.5	64.0	34	1	TYTUY2	protamine Y2 - blu
56	36	63.2	30	1	IRTR4	protamine pTP4 - r
57	36	63.2	41	2	H58208	protamine II - bla
58	35	61.4	47	2	S22828	protamine - killer
59	33	57.9	36	1	JU0352	4.6K protein - Chl
60	33	57.9	36	2	JA0173	basic peptide - wi
61	33	57.9	50	2	T30417	hypothetical prote
62	32	56.1	31	2	E70202	hypothetical prote
63	32	56.1	39	1	S28546	protamine 1 - Japa
64	32	56.1	40	1	S14717	protamine 2 - Japa
65	32	56.1	47	2	G70316	ribosomal protein

66	31	54.4	16	2	A35552	caldesmon - turkey
67	31	54.4	25	1	JC4278	ribosomal protein
68	31	54.4	25	1	R6BY4B	ribosomal protein
69	31	54.4	25	2	JQ1617	ribosomal protein
70	31	54.4	25	2	JC4685	ribosomal protein
71	31	54.4	25	2	S38425	ribosomal protein
72	31	54.4	25	2	T49214	ribosomal protein
73	31	54.4	25	2	T06233	ribosomal protein
74	31	54.4	43	2	B97505	hypothetical prote
75	29	50.9	22	2	C64330	ribosomal protein
76	29	50.9	25	2	T38719	ribosomal protein
77	29	50.9	44	2	AE2232	50S ribosomal prot
78	29	50.9	46	2	H88465	protein B0244.3 [i
79	29	50.9	47	2	C87299	hypothetical prote
80	28	49.1	23	2	S43765	ribosomal protein
81	28	49.1	48	2	A84247	hypothetical prote
82	28	49.1	49	2	T07304	hypothetical prote
83	27	47.4	27	2	I44636	homeotic protein H
84	27	47.4	39	2	I52378	gene HOX B6 protei
85	27	47.4	40	2	JC6536	interferon-gamma p
86	27	47.4	44	1	R6BS34	ribosomal protein
87	27	47.4	44	2	C48396	ribosomal protein
88	27	47.4	44	2	H97358	L34 protein [impor
89	27	47.4	45	2	A90081	50S ribosomal prot
90	26.5	46.5	18	2	PS0387	platelet-derived g
91	26	45.6	26	2	S10614	ribosomal protein
92	26	45.6	38	2	C83729	hypothetical prote
93	26	45.6	44	1	R6PS34	ribosomal protein
94	26	45.6	44	2	A82951	50S ribosomal prot
95	26	45.6	44	2	I40651	ribosomal protein
96	26	45.6	44	2	F87344	ribosomal protein
97	26	45.6	46	2	B82517	50S ribosomal prot
98	26	45.6	46	2	T16460	hypothetical prote
99	26	45.6	47	1	QQECP3	hypothetical prote
100	25	43.9	14	2	PC1215	homeotic protein E
101	25	43.9	21	2	PS0146	histone H1 - sea u
102	25	43.9	28	1	G9BPSV	gene 9 protein - s
103	25	43.9	37	1	R5LV36	ribosomal protein
104	25	43.9	40	2	A40128	probable antigen 1
105	25	43.9	42	1	QQEC45	hypothetical prote
106	25	43.9	42	2	S55687	tick embryo basic
107	25	43.9	44	2	F84645	60S ribosomal prot
108	25	43.9	45	2	S31023	gene 78 protein -
109	25	43.9	46	2	E85743	hypothetical prote
110	25	43.9	47	2	G87248	50S ribosomal prot
111	25	43.9	47	2	S70981	ribosomal protein

112	25	43.9	49	2	A37334	L-lactate dehydrog
113	24	42.1	21	2	I58423	arylhydrocarbon re
114	24	42.1	23	2	S60570	homeodomain protei
115	24	42.1	23	2	S60566	homeodomain protei
116	24	42.1	26	2	E42694	Hox 4.2 - mouse (f
117	24	42.1	27	2	I44629	homeotic protein H
118	24	42.1	27	2	G44629	homeotic protein H
119	24	42.1	27	2	F44629	homeotic protein H
120	24	42.1	27	2	A44616	homeotic protein H
121	24	42.1	27	2	H48200	homeotic protein H
122	24	42.1	27	2	G48200	homeotic protein H
123	24	42.1	27	2	F48200	homeotic protein H
124	24	42.1	27	2	B44616	homeotic protein H
125	24	42.1	27	2	F44616	homeotic protein H
126	24	42.1	27	2	G44616	homeotic protein H
127	24	42.1	27	2	I48200	homeotic protein H
128	24	42.1	27	2	G44636	homeotic protein H
129	24	42.1	27	2	F44636	homeotic protein H
130	24	42.1	29	2	S32730	homeotic protein -
131	24	42.1	29	2	S32734	homeotic protein -
132	24	42.1	29	2	S32733	homeotic protein -
133	24	42.1	33	2	A87213	hypothetical prote
134	24	42.1	34	2	I65264	homeotic protein H
135	24	42.1	37	2	F45186	homeotic protein G
136	24	42.1	42	2	S65524	antibacterial prot
137	24	42.1	42	2	I65241	homeotic protein H
138	24	42.1	44	2	AC3544	LSU ribosomal prot
139	24	42.1	44	2	A81550	hypothetical prote
140	24	42.1	45	2	E86607	L34 ribosomal prot
141	24	42.1	45	2	A72017	ribosomal protein
142	24	42.1	45	2	B84158	ribosomal protein
143	24	42.1	45	2	E71470	probable L34 ribos
144	24	42.1	45	2	PC1216	homeotic protein D
145	24	42.1	46	2	I52716	gene neu protein -
146	24	42.1	46	2	S00178	ribosomal protein
147	24	42.1	46	2	S73111	ribosomal protein
148	24	42.1	46	2	S09537	gene 1.1 protein -
149	24	42.1	46	2	B30474	homeotic protein H
150	24	42.1	49	2	S74571	hypothetical prote
151	24	42.1	50	1	R6HS39	ribosomal protein
152	24	42.1	50	2	S10907	homeotic protein (
153	23	40.4	22	2	F33084	ribosomal protein
154	23	40.4	23	2	I33084	ribosomal protein
155	23	40.4	30	2	S07217	ribosomal protein
156	23	40.4	32	2	T36275	hypothetical prote
157	23	40.4	32	2	A41270	protamine S4 - sma



158	23	40.4	33	1	WRECP1	protamine-like pro
159	23	40.4	35	2	I48897	cryptdin-15 - mous
160	23	40.4	35	2	I48896	cryptdin-13 - mous
161	23	40.4	35	2	I48891	cryptdin-8 - mouse
162	23	40.4	35	2	I48892	cryptdin-9 - mouse
163	23	40.4	37	2	E97596	hypothetical prote
164	23	40.4	38	1	GCFIK	glucagon-like pept
165	23	40.4	39	2	AE3109	hypothetical prote
166	23	40.4	41	2	S52323	major core protein
167	23	40.4	41	2	H97367	hypothetical prote
168	23	40.4	43	2	E82271	hypothetical prote
169	23	40.4	44	2	AG1431	ribosomal protein
170	23	40.4	44	2	AE1805	ribosomal protein
171	23	40.4	44	2	S52541	a 2-2 protein - in
172	23	40.4	45	2	B81733	ribosomal protein
173	23	40.4	45	2	JQ0738	ribosomal protein
174	23	40.4	46	1	R5EC34	ribosomal protein
175	23	40.4	46	2	AH0957	50s ribosomal prot
176	23	40.4	46	2	H86054	50S ribosomal subu
177	23	40.4	46	2	F91208	50S ribosomal subu
178	23	40.4	46	2	A72805	gp43.1 protein - M
179	23	40.4	47	1	JC1154	ribosomal protein
180	23	40.4	47	1	JQ0732	ribosomal protein
181	23	40.4	47	2	E84931	50S ribosomal prot
182	23	40.4	47	2	JC5557	arginine/glutamate
183	22	38.6	16	2	S05703	homeotic protein c
184	22	38.6	20	2	I55663	MHC HLA-DR gamma c
185	22	38.6	23	2	S45031	homeotic protein S
186	22	38.6	27	2	S09504	homeotic protein c
187	22	38.6	29	2	S08555	ribosomal protein
188	22	38.6	30	2	C59076	defensin alpha-3 -
189	22	38.6	33	2	I37258	NADH2 dehydrogenas
190	22	38.6	33	2	A41822	antimicrobial pept
191	22	38.6	34	2	C49195	corticostatic pept
192	22	38.6	34	2	S51069	ribosomal protein
193	22	38.6	37	2	T07519	ribosomal protein
194	22	38.6	40	2	F87419	hypothetical prote
195	22	38.6	40	2	A36605	surface-array prot
196	22	38.6	40	2	S31269	H <sup>+</sup> -exporting ATPas
197	22	38.6	41	2	B70253	hypothetical prote
198	22	38.6	41	2	F84007	hypothetical prote
199	22	38.6	42	2	S05710	homeotic protein c
200	22	38.6	43	2	PS0359	hypothetical prote

OM protein - protein search, using sw model

Run on: June 9, 2005, 14:26:31 ; Search time 72.2 Seconds  
(without alignments)  
78.018 Million cell updates/sec

Title: US-10-509-620-14  
Perfect score: 57  
Sequence: 1 YRRRRRRRRRRR 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query					Description
	Score	Match	Length	DB	ID	
1	50	87.7	37	1	PRT3_SCYCA	P30258 scyliorhinu
2	50	87.7	43	2	Q7LZB7	Q7lzb7 alligator m
3	50	87.7	45	2	Q7LZB5	Q7lzb5 chrysemys p
4	46	80.7	45	1	HSP1_CHABE	Q8wny9 chalinolobu
5	46	80.7	46	1	HSP1_MYODA	Q8wny8 myotis daub
6	46	80.7	46	2	Q64412	Q64412 cavia porce

7	46	80.7	47	1	HSP1_CAVPO	P35304 cavia porce
8	46	80.7	47	1	HSP1_EPTBR	Q8wmc7 eptesicus b
9	46	80.7	47	1	HSP1_EPTFU	Q7jh05 eptesicus f
10	46	80.7	47	1	HSP1_PLETO	Q8wnz0 plecotus to
11	46	80.7	49	1	HSP1_PLEAU	Q8wnz1 plecotus au
12	46	80.7	49	1	HSP1_SAGIM	P24714 saguinus im
13	45	78.9	24	1	HSP3_OCTVU	P83215 octopus vul
14	45	78.9	30	1	HSP5_OCTVU	P83217 octopus vul
15	45	78.9	45	2	Q7LZB0	Q7lzb0 chrysemys p
16	45	78.9	45	2	Q7LZB1	Q7lzb1 chrysemys p
17	45	78.9	47	2	Q7LZA7	Q7lza7 chrysemys p
18	45	78.9	47	2	Q7LZA9	Q7lza9 chrysemys p
19	44	77.2	21	2	Q7M3Z3	Q7m3z3 illex argen
20	44	77.2	48	1	HSP1_HIPCO	Q8wnz8 hipposidero
21	44	77.2	49	1	HSP1_PANPA	P35308 pan paniscu
22	43	75.4	32	1	PRT7_ONCMY	P08146 oncorhynchu
23	43	75.4	32	1	PRT9_ONCMY	P08147 oncorhynchu
24	43	75.4	49	1	HSP1_OTOHE	Q8wnz2 otonycteris
25	43	75.4	49	1	HSP1_SAISC	Q9gkq1 saimiri sci
26	43	75.4	50	1	HSP1_HUMAN	P04553 homo sapien
27	42	73.7	46	1	HSP1_CYNVA	Q8wp00 cynocephalu
28	42	73.7	47	1	HSP1_DESRO	Q8wme4 desmodus ro
29	42	73.7	47	1	HSP1_MONRE	Q7jh06 monophyllus
30	42	73.7	47	1	HSP1_MORME	Q8wnz5 mormoops me
31	42	73.7	47	1	HSP1_PTEPA	Q7jh07 pteronotus
32	42	73.7	48	1	HSP1_PTEHP	Q8wnz9 pteropus hy
33	42	73.7	48	1	HSP1_RHIHA	Q8wnz6 rhinopoma h
34	42	73.7	49	1	HSP1_HORSE	P15341 equus cabal
35	42	73.7	49	1	HSP1_PIG	P04101 sus scrofa
36	42	73.7	49	1	HSP1_RABIT	P10119 oryctolagus
37	42	73.7	49	1	HSP1_TRAPH	Q8mhz2 trachypithe
38	42	73.7	49	2	Q8V7C1	Q8v7c1 tt virus. o
39	42	73.7	49	2	Q8V7C2	Q8v7c2 tt virus. o
40	42	73.7	49	2	Q8V7C3	Q8v7c3 tt virus. o
41	42	73.7	50	1	HSP1_BOVIN	P02318 bos taurus
42	42	73.7	50	1	HSP1_CAPHI	P67833 capra hircu
43	42	73.7	50	1	HSP1_COLBA	Q8mjt0 colobus bad
44	42	73.7	50	1	HSP1_MACMU	Q9gju4 macaca mula
45	42	73.7	50	1	HSP1_MOUSE	P02319 mus musculu
46	42	73.7	50	1	HSP1_PAPCY	Q7jix8 papio cynoc
47	42	73.7	50	1	HSP1_RAT	P10118 rattus norv
48	42	73.7	50	1	HSP1_SHEEP	P68038 ovis aries
49	42	73.7	50	1	HSP1_TRACR	Q9gkq2 trachypithe
50	42	73.7	50	1	HSP1_TRAFR	Q9gkq4 trachypithe
51	42	73.7	50	1	HSP1_TRAGE	Q7jhm8 trachypithe
52	42	73.7	50	1	HSP1_TRAOB	Q7jix9 trachypithe

53	42	73.7	50	1	HSP1_TRAPL	Q7jhm9 trachypithe
54	42	73.7	50	2	Q66QC7	Q66qc7 equus asinu
55	42	73.7	50	2	Q8CEM2	Q8cem2 mus musculu
56	41	71.9	45	1	HSP1_EPTBN	Q8wmd3 eptesicus b
57	41	71.9	45	1	HSP1_PIPSA	Q7jh04 pipistrellu
58	41	71.9	47	1	HSP1_MURCY	Q8wny7 murina cycl
59	40	70.2	41	2	Q7LZA8	Q7lza8 elaphe obso
60	40	70.2	50	1	HSP1_HYLLA	P35306 hylobates l
61	40	70.2	50	1	HSP1_PANTR	P35309 pan troglod
62	39	68.4	27	1	PRTB_ACIGU	P02323 acipenser g
63	39	68.4	30	1	PRT1_CLUPA	P02335 clupea pall
64	39	68.4	31	1	PRT2_CLUPA	P02336 clupea pall
65	39	68.4	32	1	PRI3_ONCMY	P02330 oncorhynch
66	39	68.4	32	1	PRT1_ONCKE	P02327 oncorhynch
67	39	68.4	32	1	PRT5_ONCMY	P02334 oncorhynch
68	39	68.4	32	1	PRT6_ONCMY	P08145 oncorhynch
69	39	68.4	32	1	PRT8_ONCMY	P12817 oncorhynch
70	39	68.4	33	1	PRI2_ONCMY	P02328 oncorhynch
71	39	68.4	37	2	Q8SYH5	Q8syh5 drosophila
72	39	68.4	49	1	HSP1_NATMI	Q8wnz4 natalus mic
73	39	68.4	49	1	HSP1_NATST	Q8wnz3 natalus str
74	39	68.4	50	2	Q9GKQ0	Q9gkq0 ateles sp.
75	38	66.7	21	2	Q9JG23	Q9jg23 tt virus. o
76	38	66.7	21	2	Q9JG30	Q9jg30 tt virus. o
77	38	66.7	28	1	HSP4_OCTVU	P83216 octopus vul
78	38	66.7	30	1	PRT2_ONCMY	P02331 oncorhynch
79	38	66.7	30	1	PRT3_ONCMY	P02332 oncorhynch
80	38	66.7	30	1	PRTB_ONCMY	P12819 oncorhynch
81	38	66.7	32	1	PRT1_ESOLU	P02325 esox lucius
82	38	66.7	32	1	PRTA_ONCMY	P12818 oncorhynch
83	38	66.7	34	1	PRT_PERFV	P29629 perca flave
84	38	66.7	37	1	REV_SIVM2	P08809 simian immu
85	38	66.7	39	2	Q9PXW1	Q9pxw1 simian immu
86	38	66.7	41	2	Q7LZB3	Q7lzb3 anolis caro
87	38	66.7	49	2	O13031	O13031 cynops pyrr
88	38	66.7	50	1	HSP1_COLGU	Q9gkq5 colobus gue
89	38	66.7	50	1	HSP1_GORGO	P35303 gorilla gor
90	38	66.7	50	1	HSP1_NASLA	Q9gkq3 nasalis lar
91	38	66.7	50	1	HSP1_TRAJO	Q8mjs8 trachypithe
92	38	66.7	50	1	PRT1_SCYCA	P08433 scyliorhinu
93	38	66.7	50	2	Q7TLQ5	Q7tlq5 choristoneu
94	37.5	65.8	34	1	PRT1_SAROR	P25327 sarda orien
95	37.5	65.8	34	1	PRT1_SCOSC	P83264 scomber sco
96	37.5	65.8	34	1	PRT2_SCOSC	P83265 scomber sco
97	37.5	65.8	34	1	PRT2_THUTH	P02322 thunnus thy
98	37.5	65.8	50	1	BVCP_NPVOP	P24648 orgyia pseu

99	37	64.9	27	1	PRTA_ACIST	P02324 acipenser s
100	37	64.9	27	2	Q867D2	Q867d2 bos taurus
101	37	64.9	31	1	PRT3_CLUPA	P02337 clupea pall
102	37	64.9	33	1	PRI1_ONCMY	P02326 oncorhynchu
103	37	64.9	33	1	PRTB_MUGCE	P08130 mugil cepha
104	37	64.9	45	1	PRT2_SCYCA	P06841 scyliorhinu
105	37	64.9	47	2	Q8V7B9	Q8v7b9 tt virus. o
106	37	64.9	49	1	HSP1_SEMEN	Q9gjr3 semnopithec
107	37	64.9	49	1	HSP1_TRAVT	Q7jiy0 trachypithe
108	36.5	64.0	32	1	PRT_ORYLA	Q91185 oryzias lat
109	36.5	64.0	34	1	PRT1_THUTH	P02321 thunnus thy
110	36.5	64.0	34	1	PRT_DICLA	Q9ps27 dicentrarch
111	36.5	64.0	49	2	Q9DT80	Q9dt80 tt virus. o
112	36	63.2	30	1	PRT4_ONCMY	P02333 oncorhynchu
113	36	63.2	41	2	Q7LZA6	Q7lza6 elaphe obso
114	36	63.2	44	2	O13030	O13030 cynops pyrr
115	35	61.4	39	2	Q9PRX5	Q9prx5 xenopus lae
116	35	61.4	41	2	Q8AEX0	Q8aex0 human immun
117	35	61.4	46	1	HSP1_ORCOR	P24713 orcinus orc
118	35	61.4	50	1	HSP1_PONPY	P35310 pongo pygma
119	34	59.6	25	1	RL41_AGABI	P78569 agaricus bi
120	34	59.6	44	2	Q6SHP9	Q6shp9 uncultured
121	34	59.6	46	2	Q65X76	Q65x76 oryza sativ
122	33	57.9	21	2	Q9JG26	Q9jg26 tt virus. o
123	33	57.9	36	1	Y4KD_BPCHP	P19188 bacteriopha
124	33	57.9	36	2	Q7M1X1	Q7m1x1 cucurbita m
125	33	57.9	37	2	Q72I63	Q72i63 thermus the
126	33	57.9	48	2	Q86LB9	Q86lb9 entamoeba h
127	33	57.9	50	2	Q9YMQ8	Q9ymq8 lymantria d
128	32	56.1	13	2	Q65331	Q65331 autographa
129	32	56.1	23	2	Q94781	Q94781 trypanosoma
130	32	56.1	28	2	Q7RBX3	Q7rbx3 plasmodium
131	32	56.1	31	1	Y822_BORBU	O51762 borrelia bu
132	32	56.1	35	2	Q63896	Q63896 mus sp. nk-
133	32	56.1	39	1	PRT1_BUFJA	P24641 bufo japoni
134	32	56.1	39	1	PRT2_BUFJA	P24642 bufo japoni
135	32	56.1	40	2	Q62JK5	Q62jk5 burkholderi
136	32	56.1	44	2	Q6KF01	Q6kf01 chlamydia p
137	32	56.1	44	2	Q9MBU1	Q9mbu1 chlamydia p
138	32	56.1	47	1	RL34_AQUAE	O66563 aquifex aeo
139	31.5	55.3	22	2	Q7SIF5	Q7sif5 human immun
140	31	54.4	16	2	Q7LZ12	Q7lz12 meleagris g
141	31	54.4	23	2	Q7PF75	Q7pf75 anopheles g
142	31	54.4	25	1	RL41_ARATH	P62120 arabidopsis
143	31	54.4	25	1	RL41_CYPKA	Q6ylx4 cyprinus ca
144	31	54.4	25	1	RL41_EPICO	Q71h53 epinephelus

145	31	54.4	25	1	RL41_FELCA	P62946 felis silve
146	31	54.4	25	1	RL41_FUGRU	P62949 fugu rubrip
147	31	54.4	25	1	RL41_GOSHI	P62122 gossypium h
148	31	54.4	25	1	RL41_HORVU	P62124 hordeum vul
149	31	54.4	25	1	RL41_HUMAN	P62945 homo sapien
150	31	54.4	25	1	RL41_ICTPU	Q90ys7 ictalurus p
151	31	54.4	25	1	RL41_MOUSE	P62947 mus musculu
152	31	54.4	25	1	RL41_ORYSA	P62125 oryza sativ
153	31	54.4	25	1	RL41_PEA	P62123 pisum sativ
154	31	54.4	25	1	RL41_RAT	P62948 rattus norv
155	31	54.4	25	1	RL41_SOYBN	O49224 glycine max
156	31	54.4	25	1	RL41_SPOFR	Q7kf89 spodoptera
157	31	54.4	25	1	RL41_TOBAC	P62121 nicotiana t
158	31	54.4	25	1	RL41_YEAST	P05746 saccharomyc
159	31	54.4	25	2	Q962S2	Q962s2 drosophila
160	31	54.4	25	2	Q6B8B3	Q6b8b3 ixodes paci
161	31	54.4	43	2	Q8U5D4	Q8u5d4 agrobacteri
162	31	54.4	45	2	P72155	P72155 pseudomonas
163	31	54.4	46	2	Q50846	Q50846 methanococc
164	31	54.4	47	2	Q6VT24	Q6vt24 vibrio para
165	31	54.4	47	2	Q93S57	Q93s57 mycobacteri
166	31	54.4	47	2	Q8B8T5	Q8b8t5 human adeno
167	31	54.4	49	2	Q8WW40	Q8ww40 homo sapien
168	30.5	53.5	48	2	Q74E60	Q74e60 geobacter s
169	30	52.6	17	2	Q76N52	Q76n52 homo sapien
170	30	52.6	26	2	Q04070	Q04070 human t-lym
171	30	52.6	44	1	RL34_CLOPE	Q8xh25 clostridium
172	30	52.6	47	2	O35670	O35670 mus musculu
173	30	52.6	48	2	Q64841	Q64841 human adeno
174	30	52.6	48	2	Q6VGU8	Q6vgu8 human adeno
175	30	52.6	48	2	Q71BX0	Q71bx0 human adeno
176	29	50.9	14	1	BNCB_BENHI	P83961 benincasa h
177	29	50.9	22	1	RL41_METJA	P54025 methanococc
178	29	50.9	25	1	RL41_ASHGO	Q75ah3 ashbya goss
179	29	50.9	25	1	RL41_QUESTU	O82713 quercus sub
180	29	50.9	25	1	RL41_SCHPO	Q9y710 schizosacch
181	29	50.9	27	2	Q85G34	Q85g34 cyanidiosch
182	29	50.9	39	2	Q6LZQ0	Q6lzc0 methanococc
183	29	50.9	39	2	Q8IU49	Q8iu49 caenorhabdi
184	29	50.9	40	2	Q8WTH6	Q8wth6 epiphragma
185	29	50.9	41	2	Q8FYK8	Q8fyk8 brucella su
186	29	50.9	42	2	Q86QT7	Q86qt7 bombyx mori
187	29	50.9	42	2	Q860N1	Q860n1 rattus sp.
188	29	50.9	44	1	RL34_ANASP	Q8yrn2 anabaena sp
189	29	50.9	44	1	RL34_THEMA	P58288 thermotoga
190	29	50.9	44	2	Q8WTG8	Q8wtg8 mengenilla

191	29	50.9	47	2	Q8WTI2	Q8wti2 boreus brum
192	29	50.9	47	2	Q9AB30	Q9ab30 caulobacter
193	29	50.9	48	1	PR31_HYDCO	P83266 hydrolagus
194	29	50.9	48	1	PR32_HYDCO	P83267 hydrolagus
195	29	50.9	48	1	RL34_THEAQ	Q7x515 thermus aqu
196	29	50.9	49	2	Q6SA77	Q6sa77 bos taurus
197	29	50.9	49	2	Q9LKT3	Q9lkt3 arabidopsis
198	29	50.9	50	2	Q6XI58	Q6xi58 drosophila
199	28	49.1	9	2	Q940K4	Q940k4 arabidopsis
200	28	49.1	23	2	Q35223	Q35223 oenothera b